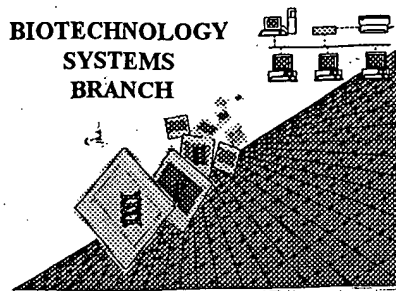


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/942,336

Source:

O/PK

Date Processed by STIC:

9/18/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/942,336

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
      Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2        Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3        Misaligned Amino  
      Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4        Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5        Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6        PatentIn 2.0  
      "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7        Skipped Sequences  
      (OLD RULES)      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
      (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
      This sequence is intentionally skipped  
  
      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8        Skipped Sequences  
      (NEW RULES)      Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
      <210> sequence id number  
      <400> sequence id number  
      000
- 9        Use of n's or Xaa's  
      (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
      In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10        Invalid <213>  
      Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11        Use of <220>      Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12        PatentIn-2.0  
      "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13        Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/942,336

DATE: 09/18/2001

TIME: 11:34:12

Input Set : A:\P02039US1.txt

Output Set: N:\CRF3\09182001\I942336.raw

Does Not Comply  
Corrected Diskette Needed

pg 1-2

OK → 3 <110> APPLICANT: Ashizawa, Tetsuo  
4       Tohru, Matsuura  
6 <120> TITLE OF INVENTION: DNA TEST FOR SCA-10  
8 <130> FILE REFERENCE: P02039US1/10023139/OTA01-01  
10 <140> CURRENT APPLICATION NUMBER: US/09/942,336  
11 <141> CURRENT FILING DATE: 2001-08-29  
13 <150> PRIOR APPLICATION NUMBER: US 60/229,406  
14 <151> PRIOR FILING DATE: 2000-08-31  
16 <160> NUMBER OF SEQ ID NOS: 13  
18 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

338 <210> SEQ ID NO: 13  
339 <211> LENGTH: 45  
340 <212> TYPE: DNA  
341 <213> ORGANISM: Mus musculus  
343 <220> FEATURE:  
344 <221> NAME/KEY: misc\_feature  
345 <222> LOCATION: (1)..(45)  
347 <400> SEQUENCE: 13  
348 cactgcagag atgagagggtc cgtgagatgg aatctgaatg tgttc  
E--> 350 25067696.1 1

45

delete at end of file

see next page

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/942,336

DATE: 10/17/2001

TIME: 10:29:16

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I942336.raw

```
155 acgagtgatg agccactcac caaggatgac atccctgtgt ttttgcggca tgctgagttg 1020
157 attgcaagca cctttgtgga tcagtgcag actgtgctca agctggcctc tgaggagcct 1080
159 cctgatgatg aggaggcact ggctacaatt aggccttctcg acgtcctgtg cgaaatgact 1140
161 gtgaatactg agctgctcgg ctatctgcag gttttccctg gcttgctgga aagagtgatt 1200
163 gatcttttgc ggggtgattca tgtagctgga aaagaaacca caaacatctt cagtaattgt 1260
165 ggttgctgga gagcagaagg tgacatctcc aatgtggcca atgggtttaa gtctcatctc 1320
167 attcgtctga ttggaaatct gtgttacaag aataaagata accaagacaa ggtaaatgag 1380
169 ctggatggta tcccgttgat cctggacaac tgcaacatca gtgacagtaa cccctttctg 1440
171 acccagtggg tgatatatgc catccgaaac cttaccgaag acaacagcca aaaccaagat 1500
173 ttgattgcaa agatggagga acaggggctg gcagatgcac ccctacttaa aaaagtgggt 1560
175 tttgaagttg aaaagaaagg cgaaaagctg atcctgaaat ctactagaga caccctaag 1620
177 ccatgaatga actacatcca aatacctgaa tttttggaat ctgtttcatg gatttttcat 1680
179 cttctaccgt atgtgaaatt gcaagtgttt gaagatttat aagtacaaat ttgggaacat 1740
181 acaaattctt taggtagtag agtttaacgt gtataagcta aaagtgaag taactgagtg 1800
183 ttctcttgtt tctttgcatt aatgtaactg tgtggtttgc ctttgtcccc ctggatagaa 1860
185 cgtgcattta aagaatatat tgtacttact gtgacagcag ataataaacc agtctcttgg 1920
187 agggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1971
```

190 <210> SEQ ID NO: 3

191 <211> LENGTH: 21

192 <212> TYPE: DNA

193 <213> ORGANISM: PRIMERS

195 <220> FEATURE:

196 <221> NAME/KEY: misc\_feature

197 <222> LOCATION: (1)..(21)

198 <223> OTHER INFORMATION: Primers

201 <400> SEQUENCE: 3

202 agaaaacaga tggcagaatg a

21

205 <210> SEQ ID NO: 4

206 <211> LENGTH: 20

207 <212> TYPE: DNA

208 <213> ORGANISM: PRIMERS

210 <220> FEATURE:

211 <221> NAME/KEY: misc\_feature

212 <222> LOCATION: (1)..(20)

213 <223> OTHER INFORMATION: Primers

216 <400> SEQUENCE: 4

217 gcctgggcaa catagagaga

20

220 <210> SEQ ID NO: 5

221 <211> LENGTH: 197

222 <212> TYPE: DNA

223 <213> ORGANISM: HUMAN

225 <400> SEQUENCE: 5

226 agaaaacaga tggcagaatg ataaactcaa tcatgttgat aaatatatta aatgtaaagtg

60

228 gcttaaatat ccaactaaaa gactactaga atggattcta ttctattcta ttctattcra

120

230 ttcrattcta ttctattcta ttctattcta ttctattcta ttctttttga gatgaagtct

180

232 ctctatgttg cccaggc

197

235 <210> SEQ ID NO: 6

236 <211> LENGTH: 20

237 <212> TYPE: DNA

*see item 10 on Env Summary Sheet*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/942,336

DATE: 09/18/2001

TIME: 11:34:13

Input Set : A:\P02039US1.txt

Output Set: N:\CRF3\09182001\I942336.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:350 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:46 SEQ:13

L:350 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9

L:350 M:252 E: No. of Seq. differs, <211>LENGTH:Input:45 Found:46 SEQ:13